

Table S9: Protein disorder abundance for completely disordered proteins.

Organism ^a	"Completely disordered" ^b		
	MD ^c	IUPred ^c	NORSnet ^c
Thermophiles			
<i>Thermosynechococcus elongatus</i> BP-1	5.8 ± 0.8	0.4 ± 0.2	0.3 ± 0.2
<i>Clostridium clariflavum</i> DSM 19732	7.2 ± 0.7	0.4 ± 0.2	0.1 ± 0.1
<i>Streptococcus thermophilus</i> LMG 18311	9 ± 1	0.7 ± 0.4	0.2 ± 0.2
Hyperthermophiles			
<i>Aeropyrum pernix</i> K1	5 ± 1	0.2 ± 0.2	0
<i>Pyrococcus horikoshii</i> OT3	4.1 ± 0.8	0.2 ± 0.2	2.1 ± 0.6
Psychrophiles			
<i>Desulfotalea psychrophila</i> LSv54	5.9 ± 0.7	0.4 ± 0.2	0.2 ± 0.2
<i>Colwellia psychrerythraea</i> 34H	8.2 ± 0.7	0.4 ± 0.2	0.08 ± 0.08
<i>Shewanella woodyi</i> ATCC 51908	5.6 ± 0.6	0.4 ± 0.2	0.2 ± 0.1
Psychrotolerants			
<i>Methanococcoides burtonii</i> DSM 6242	5.2 ± 0.9	0.3 ± 0.2	0.04 ± 0.07
<i>Leuconostoc citreum</i> KM20	8 ± 1	0.3 ± 0.2	0.4 ± 0.3
<i>Bacillus weihenstephanensis</i> KBAB4	8.6 ± 0.7	0.8 ± 0.2	0.16 ± 0.09
<i>Rhodoferax ferrireducens</i> T118	5.1 ± 0.6	0.6 ± 0.2	0.3 ± 0.1
Halophiles			
<i>Haloarcula marismortui</i> ATCC 43049	12 ± 1	4.1 ± 0.6	0.7 ± 0.2
<i>Halobacterium</i> sp. NRC-1	12 ± 1	4.1 ± 0.8	0.8 ± 0.3
<i>Marinobacter aquaeolei</i> VT8	6.6 ± 0.7	0.8 ± 0.3	0.1 ± 0.1
Alkalophile			
<i>Bacillus halodurans</i> C-125	8.1 ± 0.8	1.1 ± 0.3	0.2 ± 0.1
Radiation resistant			
<i>Deinococcus deserti</i> VCD115	4.9 ± 0.7	1.5 ± 0.4	0.8 ± 0.3
<i>Deinococcus maricopensis</i> DSM 21211	4.9 ± 0.7	1.7 ± 0.4	0.6 ± 0.3
<i>Deinococcus radiodurans</i>	6.0 ± 0.8	2.0 ± 0.5	1.0 ± 0.3
Taxonomic neighbors (mesophiles)			
<i>Caulobacter vibrioides</i>	8.1 ± 0.8	2.4 ± 0.4	1.6 ± 0.4
<i>Chromobacterium violaceum</i> ATCC 12472	7.4 ± 0.7	1.3 ± 0.3	0.7 ± 0.2
<i>Clostridium acetobutylicum</i>	7.7 ± 0.8	0.3 ± 0.2	0.10 ± 0.09
<i>Corynebacterium glutamicum</i>	6.9 ± 0.7	1.2 ± 0.3	0.5 ± 0.2
<i>Desulfovibrio vulgaris</i> str. Hildenborough	10.7 ± 0.9	2.0 ± 0.4	0.5 ± 0.2
<i>Geobacter metallireducens</i> GS-15	6.3 ± 0.8	0.4 ± 0.2	0.3 ± 0.2
<i>Geobacter sulfurreducens</i> PCA	7.4 ± 0.8	1.0 ± 0.3	0.4 ± 0.2
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	9 ± 1	0.5 ± 0.3	0.2 ± 0.2
<i>Listeria innocua</i>	8.3 ± 0.9	0.4 ± 0.2	0.1 ± 0.1

Methanosa cina mazei Go1	6.9 ± 0.8	0.5 ± 0.2	0.3 ± 0.2
Methanococcus maripaludis S2	6 ± 1	0.2 ± 0.2	0
Nitrosomonas europaea ATCC 19718	6.7 ± 0.9	0.3 ± 0.2	0.1 ± 0.1
Pseudoalteromonas atlantica T6c	4.9 ± 0.6	0.5 ± 0.2	0.2 ± 0.1
Rhodopseudomonas palustris CGA009	6.2 ± 0.6	1.3 ± 0.3	0.8 ± 0.2
Rhodospirillum rubrum ATCC 11170	6.1 ± 0.7	1.0 ± 0.3	0.6 ± 0.2
Rhodobacter sphaeroides 2.4.1	7.0 ± 0.7	1.6 ± 0.3	0.8 ± 0.2
Shewanella oneidensis	10.7 ± 0.8	0.6 ± 0.2	0.09 ± 0.08
Ruegeria pomeroyi DSS-3	4.2 ± 0.6	0.5 ± 0.2	0.8 ± 0.2
Streptomyces coelicolor	7.0 ± 0.5	2.9 ± 0.3	0.9 ± 0.2
Synechococcus elongatus PCC 6301	4.8 ± 0.8	0.4 ± 0.2	0.4 ± 0.2
Synechocystis sp. PCC 6803 substr. Kazusa	7.0 ± 0.8	0.5 ± 0.2	0.3 ± 0.2
Eukaryotes			
Arabidopsis thaliana	10.0 ± 0.3	2.3 ± 2	4.9 ± 0.2
Caenorhabditis elegans	10.3 ± 0.4	3.4 ± 0.2	5.1 ± 0.3
Dictyostelium discoideum	11.5 ± 0.5	3.2 ± 0.3	3.9 ± 0.3
Drosophila melanogaster	10.1 ± 0.4	3.2 ± 0.3	7.2 ± 0.4
Schizosaccharomyces pombe 972h-	9.2 ± 0.7	2.2 ± 0.4	3.6 ± 0.5
Saccharomyces cerevisiae S288c	8.9 ± 0.6	1.8 ± 0.3	4.3 ± 0.5

- a. Organism marks the full name of the organism where grey cells correspond to the environments; Taxonomic neighbors correspond to organisms that are related in phylogeny to the extremophiles described in this study. Eukaryotes picked at random from the set of completely sequenced organisms in UniProt.
- b. Disorder completely disordered refers to the percentage of proteins in a proteome that contains at least one region with ≥ 30 consecutive residues predicted as disordered.
- c. <MD | IUPred | NORSnet> refer to the three prediction methods used, in order to catch the different “flavors” of disorder.